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2182 2272 2362 2452 2632 2722 2812 2901

18/368 Ciossek et Figure 24

MDK1-T1

V A V A G T Î I L V P H V P G P I I G R R H C G Y S K A D O GTGGTTGTAGCAGGAACCATCATCTTGGTGTTCATGGTTTGGAAGAAGAAGAGAGCACTGTGGTTATAGCAAGGCTGACCAA 009

dustria

E G D E B L Y P H S L V T N E H L S V L . GAAGGGATGAAGAACTCTACTACTATAAACGCGGAACAACTGLLLAAGAACAAC caattitggataaacaatcaactacagcagaataaatcaagattiltaagicccatiticctitatacattcigctiatiigitgitai

attaatataaccamatatyootacctatotttytettyaaccaaatyaattyyaataotttyyaataotttattytaattyaatttyatatataay tttcaaatcactgtcatacttggtcacgggatcccaggaatattgtaaattttctaatttactctgcacttgtatatccagcctctatta ccctcaaggtgaatataaaactatgtcttttgaatatttctctttgattttgtgatagcagtccctcatatcttgtactaattttatgta atgittaittittaaacictgatcitgattgaatgigataccataagcacagitaggcigcagigtaaatatataaagacatigiiciga ttgactgagcatttatgtgttaccigcatgcttctgggtgcartgaaatattttaacttttaaaatgatactatgttgtttcaatttg gagcagtacgatttcatggaaagattgtttggtggctttgttaaaattaataaagaattttaaggatatagtgtaatttcttcattg

MDK1-T2

2002 2092 V A V A G T I I L V P M V P G P I I G R R H C G Y S K A D Q GTGGCTGTAGCAGGACCATGTGATATAGCAGGCTGACGAA

GCATCGTGCTCTCGTTTGTAGgtctcttttcctaatcaacactatgattttgaagtacgcgtacacgaagcaaacggaagaataagga

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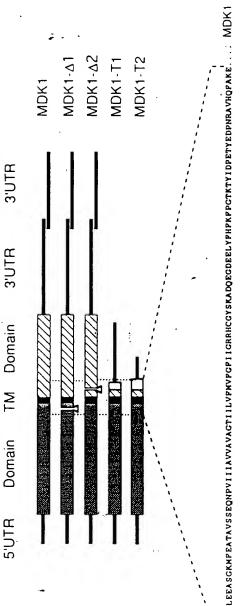
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MDK1-T1

iosseketa Fig. 28 MDK1-T2



5'UTR

Extracellular Domain

Kinase Domain

alternative 3'UTR

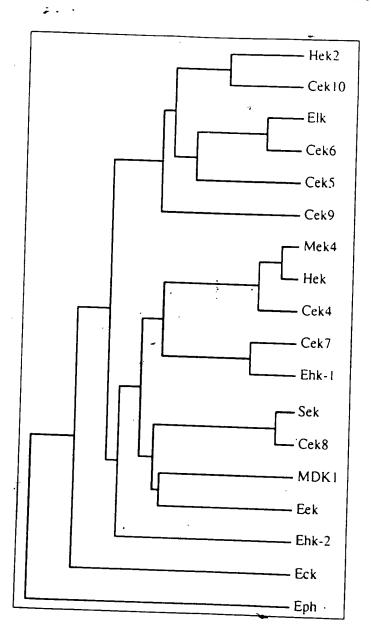
LEEAS-----ATAVSSEONPVIIIAVVAVAGTIILVPNVPGPIIGRRHCGYSKADQEGDEELYPHPKPPGTKTYIDPETYEDPNRAVHQPAKE.... MOK 1-A1

LEEASGKAPEATAVSSEQNPVIIIAVVAVAGTIILVPAVPGPIIGRRHCGYSKADQEGDEELYPHC--;-TKTYIDPETYEDPNRAVHQPAKE.... MDK1-A2

LEEA SCKMPEATA VSSEQNPVI I I AVVA VAGTI I LVPMVPGPI I GRRHCGY SKADQEGDEEL YPHSLVTNEHLSVL

LEEASGKMPEATAVSSEQNPV111AVVAVAGT11LVPMVPGP11GRRHCGYSKADQEGDEELYPHSLYRERGDGHEKTQHNKKWM1ASCSRL

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FIGURE 3

Ciossek et al.

Spinisters:

H V V Q T R P P S W I I L C T I W L L O P A H T O E A Q A A AGGITATITICITATE ACTORDATE CALCACAGGGGGAGGGCGAGGG 370 ⓒ E R ⓒ S W R Q G R ⓒ V P ⓒ G S M AGAMOTICACCENAGCAGCATOTOTOGAGCTATOGATTOTCATOTOGAGATOTATOTCTTATOGAGAAGACCTTACTOGACATO 3409 3499 3589 3628

FIGURE 1



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Abus (proje

2362 2452 2542 2632 2722 2812 2901 2002 QAAGGGGATGAAGAACTCTACTTTCATTCTTAGTAACAAATGAGCACCTGTCAGTTTTATAAGCGGGagcaataactgtttaagacaat atgittaittittaaacicigalciigaitgaatgigalaccalaagcacagitaggicgcagtgaatalalaaagacatigitciga gagcagtacgalttcatggaaagaltgitiggiggciiligitaaaaltaataaagaaltittaaggalalagiglaalticilcaligc allaalalaaccaaalalgcclaccialciilgicilgaaccaaalgaalagalliggaatacitialigaatatgaattgaattgaattgaalaag Caattitggataaacaatcaactacagcagaataaatcaagattiteaagtcccattitcctitatacattctgctattttgtcgct tticaaatcactgicatacttggicacggatcccaggaatattgtaaattictcaatttactctgcactttgtatatccagcctctatca ccctcaaggigaatataaaactatgicttittgaatatticictttgabtttgggaagagcagtccctcatatcttgtaatttitatgta tigacigagcatttatgigttaccigcatgcttcigggigcatigaaatatttaactittaaaatgataciatgitgticaatitiga CLACCELETY GAGGCALACT GGC LCCECCEL CELEGE LA GAGGE LCETE CCA A GAGGC LE LA GAGA A A GET LA LA LA LA CALECE C 610 J EGDEELYPИS LVTNEHLSV 900

MDK1-T2

V A V A G T I I L V P M V P G P I I G R R H C G Y S K A D O GFGGCFGFAGGACCATCATGATGTTCATGGTGTTCATCATCATTGAAAAAGGCACTGTGGTTATAGCAAGGCTGACCAA GHERTOHNRKK 610 E E L Y P H S L Y R E R G D O

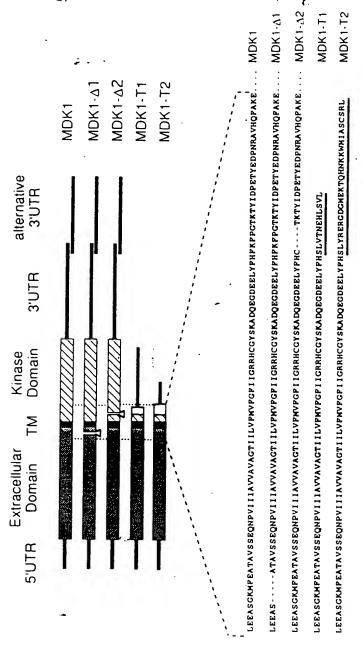
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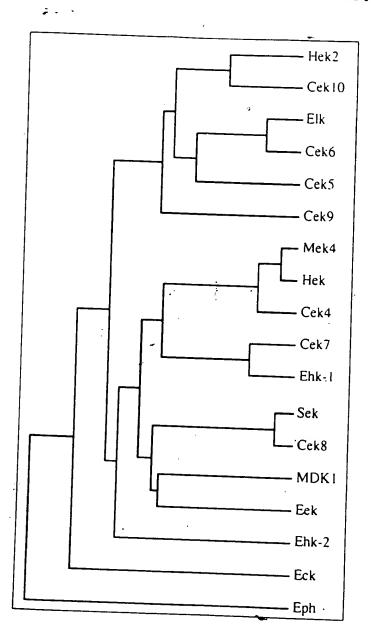
2272 2182 attagcattgtgaacctgactgtaatcctcttcctggaaagagatgatgctattgcgatgagaatgtacaacttgcaccttgaaatc A S C S R L * GCATCGTCTCGTTTGTAGgtctctttcctaatcaacactatgattttgaagfacgcgtacacgaagcaaacgggaagaqataagga tttttgataattagtgeteaggggaggggggggaagtagagaaageaaa

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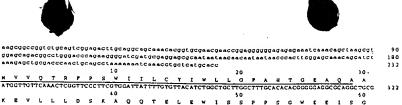
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FIGURE 3

Ciossek et al.



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aagdggcagtusuusussa ggggnategaagaggagcaataata
ggagcagaacggcagtgcagcaagaanatcaaacctggtcatgcacc
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H V V O T R P P S W I I L C Y I W L 3229 cacatrogocticoctoagatgagoctiaagactgoaggagaacagtictggocticagtalacgoalagaatgotgolagaagacagtig alalactgogtocticolacaagaagagaagattilagaagoacoticoagactigaactoctaaggococcagaalalacaaaaago aatillaggalocoacocctgygigoologgaacaagoagagacaalaaagaaglaclactgaaaacatoocaacacotigaacacacottigaoctoco aacoloctilitalotialagactittiaaaaatgiagalaaagaaltlaagaaagaalalattigocaactaaaaacacotgacticat 3679 3769 3859



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		2002			2092
065	VAVAGTIILVPMVPGPIIGRRHCGYSKADO	GTGGCTGTAGCAGGACCATCATCTTGGTGTTCATGGTGTTCGGCTTCATCATTGGAAGAAGCACTGTGGTTATAGCAAGGCTGACCAA. 2002			GAAGGGGATGAAGAACTCTACTTTCATTCTTAGTAACAAATGAGCACCTGTCAGTTTTATAAaccgcaacaataactgtttaagacaat 2092
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580	ပ	GGA	61	>	GTT
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	Ö	366		ω	SAC
	۲a	TTC		z	AA
	>	GTC		F	ACZ
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	Δ,	TTC		L	LL
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'n	J	TT	9	H	CAT
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2632 2182 2272 2362 1452 2542 2722 2812 2901 caattttggataaacaatcaactacagcagaataaatcaagatttttaagtcccattttcctttatacattctgcttattttgttgttgttat atgtttattttttaaactctgatcttgattgaatgtgataccataagcacagttaggctgcagtgtaaatataaaagacattgttctga gagcagtacgatttcatggaaagattgtttggtggctttgttaaaattaataaagaatttttaaggatatagggtaattttcttcttcattgc ctaccttttgtgaggcatactggctacctcctattagctaagatcttccaaagccttataatgaaaagtttatataaaccatttctc attaatataaccaaatatgcctacctatctttgrcttgaaccaaatgaatagatttggaatactttattgtaattgaaattgatataaag ttgactgagcatttatgtgttacc.gcatgcttctgggtgcattgaaatattttaacttttaaatgatactatgttgtttcaattttga tttcaaatcactgtcatacttggtcacggatcccaggaatattgtaaattttctaatttactctgcactttgtatatccagcctctatta coctcaaggtgaatataaaactatgtcttttgaatatttctctttgattttgtgatagcagtccctcatatcttgtactaattttatgta

MDK1-T2

		2002			2092
590	VAVAGTIILVPMVPGP.I.IGRRHCGYSKADO	9TGGCTGTAGCAGGGACCATCATCTTGGTGTTTCATGGTGTTTCGGCTTCATCATTGGAAGGAA	620	EGDEELYPHSLYRERGDGMEKTQHNKKWMI	GAAGGGGATGAAGAACTCTACTTTCATTCTCTTTACAGGGAAAGGGGAGACGGGATGGAAAAGACACACAAAAAGAAGAAGAAGAAGAAGAAGAAG
	4	AGG		3	AGT
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	Сц	TI		ဗ	99
	O	9		~	AGG
	ы	STTC		Б	SGAA
	>	3GT		æ	,AG
	Σ	SATC		>-	LTAC
	ы	TT		ᆈ	CT
570	>	3616	009	S	FTCT
'n	L	TT	9	H	CAS
	H	CATC		М	CTT
	н	CAT		×	TA
	۲	GAC		'n	ACTO
	O	AGG		囟	AGA
	K	AGC		ы	TGA
	>	TGT		Ω	GGA
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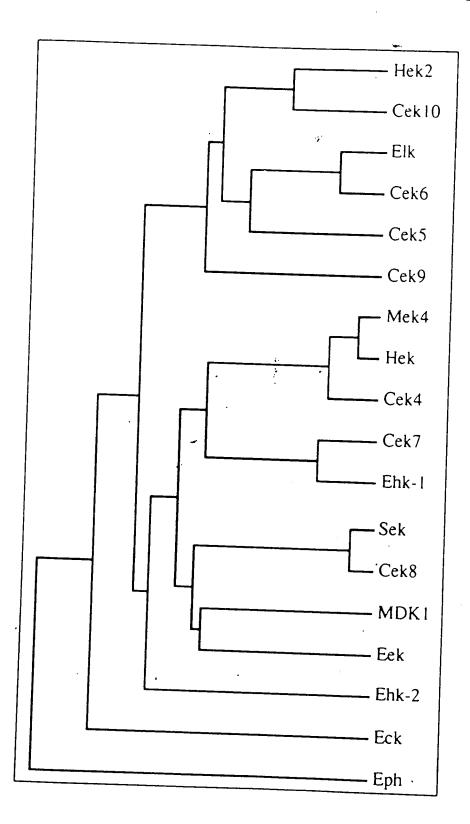
iossek et Fig. 2B

alternative 3'UTR 3'UTR Kinase Domain ≥ Extracellular Domain

MDK1-Δ2 MDK1-T1 MDK1-_Δ1 MDK1-T2 MDK1

LEEASGKMPEATAVSSEQNPVIIIAVVAVAGTIILVPMVPGPIIGRRHCGYSKADQEGDEELYPHC----TKTYIDPETYEDPNRAVHQPAKE.... MDK1-A2 MDK1-T2 LEEAS----ATAVSSEQNPVIIIAVVAVAGTIILVPMVPGPIIGRRHCGYSKADQEGDEELYPHPKPPGTKTYIDPETYEDPNRAVHQPAKE....MDK1-Δ1 MDK1-T1 LEEASGKMPEATAVSSEQNPVIIIAVVAVAGTIILVPMVPGPIIGRRHCGYSKADQEGDEELYPHPKPPGTKTYIDPETYEDPNRAVHQPAKE... MDK1 LEEASGKMPEATAVSSEQNPVIIIAVVAVAGTIILVPMVPGPIIGRRHCGYSKADQEGDEELYPHSLYRERGDGMEKTQHNKKWMIASCSRL LEEA SGKMPEATAVS SEQNPVIIIAVVAVAGTIILVPMVPGPIIGRRHCGY SKADQEGDEELYPHSLVTNEHLSVL

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FIGURE 3